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RESULT 1
Q920KS
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Q920KS;
Q1-DEC-2001 (TERMELrel. 19, Created)
Q1-DEC-2001 (TERMELrel. 19, Last sequence update)
Q5-UTL-2004 (TERMELrel. 27, Last annotation update)
Q5-UTL-2004 (TERMELrel. 27, Last annotation update)
Dem-A20-4 (BALC: 1soform 1-6-8).
Name-dem-A20-4; Synonyms-Baalc;
Rattus norvegicus (Rat).
Bukaryota; Metezoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metezoa; Chordata; Sciurognathi; Muridae; Murinae; Rattus.
SEQUENCE PROM N.A.
STRALN=Sprague-Dawley;
MEDILINE-21574584; PubMed-11707601;
Tannar A M Buerta II.
                                                                                                                                            SEQUENCE FROM N.A. Wang X., Tian Q., Li Submitted (OCT-2001)
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Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 00
Maximum Match 1000

Listing first 45 summaries

Database: Uniprot_02:*
1: uniprot_trembl:*
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2: uniprot_trembl:*
3: uniprot_trembl:*
2: uniprot_trembl:*
3: uniprot_trembl

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Finance: Sequence:

US-10-705-716A-22

MGCGGGRADAIBPRYYBSWT.....VTENIRQMDRSKRVTKNCIN 145

OM protein

protein search, using sw model

GenCore version 5.1.6 Compugen Ltd.

November 17, 2004, 14:59:59; Bearch time 103.667 Seconds (without alignments)
804.784 Million cell updates/sec

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PRT; 145 AA.	KRYTENCIN 145	SVAISVTENIROMDRSKRYTKNCIN 145	SSNGVLRPAAPGGIANPEKRANCGTQCPNSQSL86GPLTQXQNGLWTTEAKRDAKRASAR 120	SSNGVLRPAAPGGTANPEKKUNCGTQCPNSQSLSSGPLTQKQNGLWTTBAKRDAKRMSAR 120	MGCGGSRADAIEPRYYESWIRETESIWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60	1 MGCGGSRADAIEPRYYESWTRETESTWITYTDSDALPSAAATDSGPEAGGIHAGVLEDGF 60	0; Mismatches 0; Indels 0; Gaps 0;	100.0%; Score 767; DB 2; Length 145; 100.0%; Pred. No. 3.4e-61;	5 MW; D5A27AD67456F341 CRC64)		C. N.		Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).	lineage, is implicated in hematopoiesis and acute leukemia.";	*BAALC, the human member of a novel mammalian neuroactodarm gane	Caligiuri M.A. Bloomfield C.D. de la Chapelle A.

1 767 100.0 145
2 746 97.3 145
3 645 82.7 145
4 634 82.7 145
5 61.5 80.5 180
6 473.5 80.5 180
7 459 59.8 123
7 459 138.3 54
10 288 37.5 73
11 278 36.2 54
12 278 36.2 54
13 272 35.5 80
14 267 34.8 54
15 12 10 32
16 92.5 12.1 613
18 92.5 12.1 613
18 92.5 12.1 73
19 92.5 12.1 1073
20 89.5 11.3 1073
20 89.5 11.3 1035
22 87 11.3 1035
24 87 11.3 1713
25 887 11.3 1713
26 86 11.2 1070
27 86 11.2 1070
28 94.5 11.0 534
29 84.5 11.0 534
29 84 11.0 155

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SEQUENCE FROM N.A.

STRAIN=C57BL/65; TISSUE=Cerebellum;
MEDLINE=9279253; PubMed=10349636;

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303;19-44(1999).

[3]
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MEDLINBs21574584, PubMed=11707601,
MEDLINBs21574584, PubMed=11707601,
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
Rrozek K., Sill H., Knuutila S., Kolitz J.S., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.,
"BAALC, the human member of a novel mammalian neurosctoderm gene
"BAALC, the human member of a novel mammalian neurosctoderm gene
"Ilineage, is implicated in hematopolesis and acute leukemia.",
Proc. Natl. Acad. Sci. U.S.A. 98113901-13906(2001).
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01-MAR-2002 (TREMELTel. 20, Last sequence update)
01-MAR-2002 (TREMELTel. 28, Last sequence update)
01-CCT-2004 (TREMELTel. 28, Last amotation update)
BAACC isoform 1-6-8 (Mus musculus 16 days neonate cerebellum cDNA,
RIKEN full-length enriched library, clome:9630028H16 product:brain
acute leukemia, cytoplasmic, full insert sequence).
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STRAIN-C57BL/6J; TISSUE-Cerebellum;
MEDLINE-2186560; PubMed-11217851;
RIKEN PANTOM Consortium;
*Punctional annotation of a full-length mouse
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Mus musculus (Mouse)
Chordata;
Metaica; Rodentia;
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STRAIRS-C57BL/6J, TISSUE-Cerebellum;
STRAIRS-C57BL/6J, TISSUE-Cerebellum;
MEDILINE-20530913, PubMed-11076861;
Shibata K., Itoh M., Aisawa K., Magacka S., Sasaki N., Carninci P.,
Schibata K., Itoh M., Aisawa K., Kitsunai T., Tashiro H., Itoh M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro T., Harada A.,
Sumi M., Ishi Y., Wakamura S., Hesama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikogami T., Kashiwagi K.,
Pujiwake S., Incue K., Togawa Y., Izawa C., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okaraki Y., Muramatsu M., Incue Y., Kira A., Hayashizki Y.,
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 mmliticapillary sequencer.",
Genome Res. 10:1757-1771(2000).
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STRAIN=C578L/6J; TIBSUE=Cerebellum;

The FANTOM Consortium,

the RIEEN Genome Exploration Research Group

"Analysis of the mouse transcriptome based of 60,770 full-leagth CDWAs.";

Nature 420:563-573(2002).
SEQUENCE FROM N.A.

STRAIN=C57EL/6J; TISSUE-Cerebellum;
Adachi J., Airawa K., Akimura T., Arakawa T., Bono
Pukuda S., Furuno M., Hanagaki T., Hara A., Hashiw
Hayashida K., Hayateu N., Hiramoto K., Hiraoka T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I.,
                                                                                                                                                                                                                                                                                                                                                                                                                           ÉBQUENCE FROM N.A.

ÉTRALIN=C57BL/6J; TISSUE=Cerebellum;

BETRALIN=267BL/6J; TISSUE=Cerebellum;

MEDILINE=20499374; PubMed=11042159;

Carninoi P., Shibata Y., Hayatau N., Sugahara Y., Shibata K.,

Konno H., Okaraki Y., Murematsu M., Hayashiraki Y.;

*Normalization and subtraction of cep-trapper-selected cDNAs to prepare full-length cDNA libraties for rapid discovery of new Genome Res. 10:1617-1630(2000).
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Sciurognathi; Muridae; Murinae; Mus
    T., Bono H., Carminci
., Hashisume W.,
raoka T., Hirozane T.,
agawa I., Kasukawa T.,
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RA Nishi K., Nomura K., Mumaraki R., Murata M., Nakamura M., Raitoh H., Sakai C., Sakai K., Bahato R., Sakai Y.,
RA Gasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takahu-akahira S., Takeda Y.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashiraki T.,
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL, AR079137; BAJ50516.1; -.
DR EMBL, AR079137; BAJ50516.1; -.
DR MGD, MGI11928704; Bealc.
NR InterPro; IPR009728; BAJLC_N.
R Pfam, PP06989; BAJLC_N.
R Pfam, PP06989; BAJLC_N.
SEQUENCE 145 AA; IS515 MM, 4972670A618674767
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RA CLATE, VALUE V., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Rakamatsu A., Hayashi K., Bato H., Nagai K., Kimura K., Nakita H., Ra Sakine M., Obayashi M., Nishi T., Shibahasa T., Tanaka T., Ishii S., Ra Sakine M., Obayashi M., Nishi T., Shibahasa T., Tanaka T., Ishii S., Ra Sakine M., Obayashi M., Nishi T., Isono Y., Nakamura Y., Nagahari K., Ra Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Ra Yamamoto J., Saito K., Isono Y., Nakamura Y., Nagahari K., Ra Yamamoto J., Saito K., Nagatsuma M., Shiratori A., Ra Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Ra Sudo H., Hosoiri T., Yamashita H., Kurakawa S., Omura Y., Ra Ninomiya K., Ishibasahi T., Yamashita H., Nurakawa M., Yamasaki M., Arita M., Ishida S., Ra Yamashi H., Kimata M., Hara H., Tanaso T., Nomura Y., Ra Yosiikawa Y., Matanabe S., Yosida M., Hotsuka S., Yosiika N., Arita M., Imosa N., Yamasaki M., Matanabe T., Shiohata N., Bano S., Yoshikawa Y., Matanabe T., Shiohata N., Baso S., Yoshikawa Y., Matanabe T., Shiohata N., Baso S., Yoshikawa Y., Matanabe T., Sugiyama A., Takemoto M., Kwakami S., Torashima Y., Wakaswa S., Senoh A., Minagai A., Takemoto M., Kwakami Y., Ra Hishigaki H., Matanabe T., Sugiyama A., Takemoto M., Kwakami Y., Yamasaki M., Matanabe T., Sugiyama A., Takemoto M., Kwakami Y., Yamasaki M., Matanabe T., Sugiyama A., Takemoto M., Kwakami Y., Yamasaki M., Matanabe T., Sugiyama A., Takemoto M., Kwakami Y., Yamasaki M., Matanabe T., Sugiyama A., Takemoto M., Kwakami Y., Yamasaki M., Matanabe T., Sugiyama A., Takemoto M., Kwakami Y., Yamasaki M., Hikiji T., Xobatake N., Hikio M., Okamoto S., Khima Y., Okamoto S., Khima R., Khima Y., Okamoto S., Khima R., Khima Y., Okamoto S., Khima R., Hikiji T., Xobatake N., Inagaki H., Ikema Y., Okamoto S.,
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Matches 141
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01-MAR-2001 (TrEMBirel. 16, Last enquence update)
01-0CT-2004 (TrEMBirel. 28, Last enquence update)
Hypothetical protein FLJ12015 (BAALC isoform 1-6-8)
1sukemia, Cytoplasmic) (BAALC 1-6-8)
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Bukaryota, Metazoa,
Mammalia, Butheria,
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al Similarity 297.43%;
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2; Mismatches
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